

Docket No.: 7682-109-999 Serial No.: 10/722,050

Inventor(s): Spaete et al.

Title: "NON-SPLICING VARIANTS OF GP350/220"

- MetGluAlaAlaLeuLeuValCysGlnTyrThrIleGlnSerLevIleHisLevThrGly 20 -900 TCTGTACAATGTTACCCACGGAGCTCTGAACATACAACCACTGGCGATCCCCGGGGTACATCGCGGCAGCTTAAAGGTGCCGGCGGAAAAGGTCACGTGACATGTACGGCCACCTGTGC -780 ACCCAAGTGTCGCCTGGAGATGTAGGAATGTGGGAGTCGTCTGGTGATCGGTGTAGCTGTACATCCAGCTGCTGTATGCCCTGGTAGGCCATAGGCCATCCGGCGGGGTTTGCAGTC -660 ICCATTIGGCCTGATCTCTACGAGAAGCTGGATTICTCCGACGATCTCTAATGGCCTGTCGAATGGCCATGGCCATACATTAIGTACATCTCGGTATTTGAAATCTGGAATACCGAAAAAACTG -420 CGCCTCCAATCGCTTGAAGAAGTGTTCTTAGATCTAGTGGAAACCTGCGGAGAATGGCTTCTCGCCCAGGGAGATCCGGCTGGGGTGGGAGCATGGGTCGTGCTGGAGCTGACCCACGG -180 CCGATACCTGTTCCTGCACAACCGAGGTAGATGGGACTTCTTCTTCTTGTGTTGTCAGGGCGGGGGGCCGGGCTGTCCTTGTCCATTTTGTCTGCAACAAAGTGTGACTCACCA -1013 EcoR] CAATTCCATAAATGAAACACGCTGGTCAGGTGTTAAAACTTCCTCCCAGATTTTCGTGAGGCTCCTGTGTATAGCCATATAGTCAAAGAAAATACTGTAGCGGGATTACAGC -300 CATCATGATCGACCCGCTTTCTCTTCGTACCCTTCTGGGCCGGCTCCAGGTGGGCATCTTCTGCTTTTCTGAGCTGCTATCTGATAAC†CTATGAGGACATTTTCCCAATCTCCCG
- GluAspProGlyPhePheAsnValGluIleProGluPheProPheTyrProThrCysAsnValCysThrAlaAspValAsnValThrIleAsnPheAspValGlyGlyLysLysHisGln 60 61 GAAGATCCTGGTTTTTCAATGTTGAGATTCCGGAATTCCCATTTTACCCCACATGTTTGCACGCCAGATGTTGCAATGTATTTCGATGTTGGATGTTTCGATGTTGGATGTTTCGATGTTGGAAAAGCATCAA
- LeuAspLeuAspPheG1yG1nLeuThrProHisThrLysA1aVa1TyrG1nProArgG1yA1aPheG1yG1ySerG1uAsnA1aThrAsnLeuPheLeuLeuG1uLeuLeuG1yA1aG1y 100 CITGAICTIGACTITGCCCAGCTGACACCCCATACGAAGGCTGTCTACCAACCTCGAGGTGCATTIGGTGGCTCAGAAAATGCCACCAATCTCTTCTACTGCAGCTCCTTGGTGCAGGA <u>2</u>
- GluLeuAlaLeuThrMetArgSerLysLysLeuProIleAsnValThrThrGlyGluGluGlnGinValSerLeuGluSerValAspValTyrPheGInAspValPheGlyThrMetTrp 140 301 GAATIGGCICTAACTAIGCGGTCTAAGAAGCTICCAATIAACGICACCACCGCGAGAGCAACAACTAAGCCTGGAATCTGTAGATGTTTCAAGATGTGTTTGGAACCAIGTGG
- CysHisHisAlaGluMetGlnAsnProValTyrLeuIleProGluThrValProTyrIleLysTrpAspAsnCysAsnSerThrAsnIleThrAlaValValArgAlaGlnGlyLeuAsp 180
- VolThrLeuProLeuSerLeuProThrSerAlaGlnAspSerAsnPheSerValLysThrGluMetLeuGlyAsnGlulleAsplleGluCysIleMetGluAspGlyGlulleSerGln 220 541 GTCACCCTACCCTTAAGTTTGCCAACGTCAGCTCCAAGACTCGCAATTTCAGCGTAAAAACAGAAATGCTCGGTAATGAGATATTGAGTGTATTATGGAGGATGGCGAAATTTCACAA
- ValLeuProGIyAspAsnLysPheAsnIIeThrCysSerGIyTyrGIuSerHisVaIProSerGIyGIyIIeLeuThrSerThrSerProVaIAIaThrProIIeProGIyThrGIyTyr 260 661 GTICTGCCCCGACAACAACAATTAACATCACCTGCAGTGCATACGAGAGCCATGTTCCCAGCGGCGGAATTCTCACATCAACGAGTCCCCTGGCCCCAATACCTGGTACAGGGTAT

- SerAsnileVoiPheSerAspGluileProAlaSerGinAspMetProThrAsnThrThrAspileThrTyrVaiGlyAspAsnAlaThrTyrSerVaiProMetVaiThrSerGiuAsp 340 TCCAACATIGITICICIGATGAGATTCCAGCTTCACAGGACATGCCGACAAACACCACAGACATCACATATGTGGGGTGACAATGCTACTATTCAGTGCCAATGGTCACTTCTGAGGAC
- 380 AlaAsnSerProAsnValThrValThrAlaPheTrpAlaTrpProAsnAsnThrGluThrAspPheLysCysLysTrpThrLeuThrSerGlyThrProSerGlyCysGluAsnIleSer 021 GCAAACTCGCCAAATGTTACAGTGACTGCCTTTTGGGCCTGGCCAAACAACACTGAAACTGACTTTAAGTGCAAATGGACTCTCACCTCGGGACACCTTCGGGTTGTGAAATATTTCT
- GiyAlaPheAlaSerAsnArgThrPheAspileThrValSerGiyLeuGlyThrAlaProLysThrLeuIleIleThrArgThrAlaThrAsnAlaThrThrThrThrHisLysValIle 420 141 GGTGCATTIGCGAGCAATGGGACATTIGACATTACTGTCTGGGGTCTTGGCACGCCCCCAAGACACTCATTATCACACGAAGGCTACCAATGCCACCACCAACAACAAGGTTATA
- PheSerLysAloProGluSerThrThrSerProThrLeuAsnThrThrGlyPheAlaAspProAsnThrThrGlyLeuProSerSerThrHisVa1ProThrAsnLeuThrAla 460 261 TICTCCAAGGCACCCCAGAGCACCACCTCCCCTACCTIGAATACAACTGGATTTGCTGATCCCAATACAACGACGACGTCTACCCAGCTCTACTACGAGGTGCCTACCAACCTCACCGCA
- ProAlaSerThrGlyProThrValSerThrAlaAspValThrSerProThrProAlaGlyThrThrSerGlyAlaSerProValThrProSerProSerProTrpAspAsnGlyThrGlu 500 CCTGCAAGCACAGGCCCCACTGTATCCACCGCGGATGTCACCAGCCCCAACACACAGCGGCACAACGTCAGGCGCATCACCGGTGACAAGTCCATGTCCATGGGACAACGGCACAGGAA 381
- 540 SerlysAalProAspMetThrSerSerThrSerProValThrProThrProAsnAlaThrSerProThrProAlaValThrThrProThrProAsnAlaThrSerProThrProAla 501
- ValThrThrProAsnAlaThrSerProThrLeuGlyLysThrSerProThrSerAlaValThrThrProAsnAlaThrSerProThrLeuGlyLysThrSerProThr 580 621
- 620 SerAlayal Thr ThrProIhrProAsnAlaThrSerProThrLeuGlyLysThrSerProThrSerAlayal Thr ThrProAsnAlaThrGlyProThrValGlyGluThrSer TCAGCAGTGACTACCCCAACCCCAAATGCCACCACCACCTTGGGAAAAACAAGCCCCACCTCAGCAGTGACTACCCCAACCCCAAATGCCACCGGCCCTACTGTGGGAAACAAGT 741
- 99 ProGInAlaAsnAlaThrAsnHisThrLeuGlyGlyThrSerProThrProValValThrSerGlnProLysAsnAlaThrSerAlaValThrThrGlyGlnHisAsn1leThrSerSer CCACAGGCAAATGCCACCACCACACCTTAGGAGGAACAAGTCCCACCCCAGTAGTTACCAGCCAAAAAAATGCAACCAGTGCTGTTACCACAGGCCAACATAACATAACTTCAAGT 861

ATICICEIGEICEICEITCCCICACCAGGGCTGGCTTTGCCCTTTTGCACCCAACATAGATACTTGAATGCGGAGGGTCAGATTTTGCAATATTTTCCATTTCATTGCGGGTAGTTACACACA AATCCGTCAGCAGCGTGFTCACAAACTTGTTAAAGCAGACGTACATCAGGTAGATGGCTGAGGCTATAATGACTAAGACAAGCCTCAGAAGTGCCCAGATGGAGGCCAAAAGCTGGTGGTGGTGGAGGCTAAAG TGTCTGTTAGATCATCACCATGGAGGCCTGTCCACACATACGCTACGCCTTCCAGAATGACAAGCTGTTGCTCCAGCAGGCTAGTGTAGGGCGGCTCACCTTGGTCAACAAGACCACAT TGTCAACAGCCTTAACAGAAGGCAATCTGACTTTGCGTGGAGCTGACATGCTTTAACGAGCAGAGAAGAAGTACAAACAGCCCGAGATTGCTGCCCCTTTTAAATATCCCCATCT 3421

POLYA

AspAspAloGluThrTyrVal\*\*\*

FIG. 10

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AGGCACCGGTCTCGTCCATCTTGAGCGCCGTGCCCATCTCCCATCTCCCATCAGGCCCAGGCCTGTCGCCAGCCTGTTGTCCAGCGCCCTTGAGCCCATTCTCGTCCATCTCGATCC CATCGATCCCGGCTACACGGGGGAACTCCGGGCTAATCCTCCAGAATCAGGGGGCTACAACTCCACGCTGCGTCCATCGGAGCTCAAAATCCACCTGGCTGCCTTCAGATATGCCACCC CACCETECCCCCCCTTCTATCCCTCACCACAGGCCGACAATCTTTGGCAGGTCGGGCCTGGCCATGCAGGGTATTCTAGTGAAGCCCTGCAGGTGGCCCGGGGTGGGGTTGGGGTGGGGTGGGGTTCAG CCTGACCAACTTTAGTGACCAGACCGTGTTCCTTAACAAGTACCGGCGCTTCTGTCAGCTTGTTTACCTTCACAAGCACCACCTCCCTTCTACAGCCCCCACAGTGACGCGGGGGGT CCTTGCCCCCAGATCTCTCTTTAGGTGGGCCAGCTGCACCTTCGAGGAGGTGCCGAGGCTGGCCATGGGTGATAGTGGGCTGAGCGAGGCGCTCGAGGGGAGACAGGGGGAGGGGGGTTTTGG CCAGATGGAGGAGGACAAGGGTCCCATCAACCACCCCCAGTACCCCGGGGACGTGGGCCTGGACGTCTTTGCCAAAGGACCTGGCCCTCTTCCCCATCAGACGGTCTCAGTGACACT CGCTTACAGCCAGAGAGATCATGGTATTCCAGATGACTGAGCGCCACGGCCTCAAGCTT HINDIII 4021 4141 4261 4501 4381

FIG. 1D



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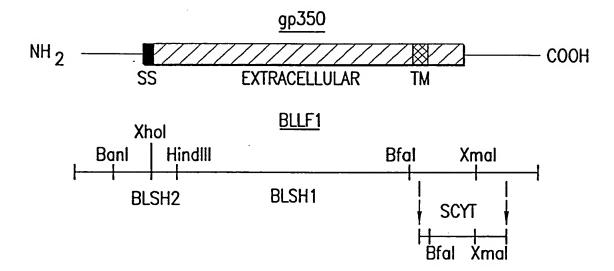


FIG. 2A

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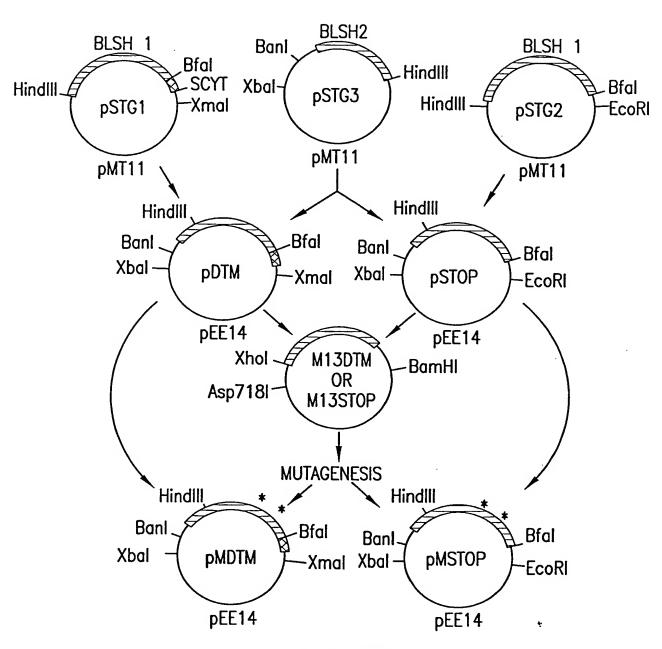


FIG. 2B

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